#2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/988,201

DATE: 01/15/2002
TIME: 19:00:24

Input Set : N:\Crf3\RULE60\09988201.raw
Output Set: N:\CRF3\01152002\I988201.raw

SEQUENCE LISTING

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 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: BARBEYRON, Tristan
 6                     POTIN, Philippe
 7                     RICHARD, Christophe
 8                     HENRISSAT, Bernard
 9                     YVIN, Jean-Claude
10                     KLOAREG, Bernard
13     (ii) TITLE OF INVENTION: Glycolyse hydrolase genes and their
14                              use for producing enzymes for the biodegradation of
15                              carrageenans
17    (iii) NUMBER OF SEQUENCES: 8
19     (iv) CORRESPONDENCE ADDRESS:
20          (A) ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
21          (B) STREET: 612 Crystal Square 4, 1745 Jefferson Davis
22                      Highway
23          (C) CITY: ARLINGTON
24          (D) STATE: VIRGINIA
25          (E) COUNTRY: U.S.A.
26          (F) ZIP: 22202
28      (v) COMPUTER READABLE FORM:
29          (A) MEDIUM TYPE: Floppy disk
30          (B) COMPUTER: IBM PC compatible
31          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
32          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
34     (vi) CURRENT APPLICATION DATA:
C--> 35         (A) APPLICATION NUMBER: US/09/988,201
C--> 36         (B) FILING DATE: 19-Nov-2001
37              (C) CLASSIFICATION:
43    (vii) PRIOR APPLICATION DATA:
40              (A) APPLICATION NUMBER: 09/269,731
41              (B) FILING DATE:
44              (A) APPLICATION NUMBER: FR 96 12204
45              (B) FILING DATE: 07-OCT-1996
47   (viii) ATTORNEY/AGENT INFORMATION:
48              (A) NAME: IRA SCHULTZ
49              (B) REGISTRATION NUMBER:
50              (C) REFERENCE/DOCKET NUMBER:
52     (ix) TELECOMMUNICATION INFORMATION:
53              (A) TELEPHONE: (703) 412-1155
54              (B) TELEFAX: (703) 412-1161
56 (2) INFORMATION FOR SEQ ID NO: 1:
58      (i) SEQUENCE CHARACTERISTICS:
59              (A) LENGTH: 2085 base pairs
60              (B) TYPE: nucleic acid
61              (C) STRANDEDNESS: single
62              (D) TOPOLOGY: linear
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ENTERED

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64      (ii) MOLECULE TYPE: DNA (genomic)
66     (iii) HYPOTHETICAL: NO
70      (ix) FEATURE:
71            (A) NAME/KEY: CDS
72            (B) LOCATION:join(211..1683, 1880..2083)
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 AAGCTTTCCG ATTCTATCAT CGAAGTCATA GGAGTGGGTA AACAAAAAAG CATGAAACTA      60
77 GCTTTTTAAA ATACAGACTT TCAATATAGG TCGCACACAA TATTAACGAA TAAATAAGCA     120
78 AATCATATAC ATAATCATTG CTTTAAATAT GTTTAATAC AGATATAAAC ATAGTATGTT      180
79 TGTGTTTTTG GTATCTATCG GAGTGAAAAC ATG CGC TTA TAT TTT AGA AAG TTG     234
80                                  Met Arg Leu Tyr Phe Arg Lys Leu
81                                   1               5
83 TGG TTA ACA AAT TTA TTT TTA GGC GGA GCA CTG GCC TCT TCA GCT GCG     282
84 Trp Leu Thr Asn Leu Phe Leu Gly Gly Ala Leu Ala Ser Ser Ala Ala
85     10              15                  20
87 ATA GGG GCT GTC TCC CCC AAG ACT TAT AAG GAC GCA GAT TTT TAT GTT     330
88 Ile Gly Ala Val Ser Pro Lys Thr Tyr Lys Asp Ala Asp Phe Tyr Val
89 25              30                  35                  40
91 GCC CCT ACT CAA CAA GAT GTT AAC TAT GAT TTA GTT GAT GAT TTT GGC     378
92 Ala Pro Thr Gln Gln Asp Val Asn Tyr Asp Leu Val Asp Asp Phe Gly
93                 45                  50                  55
95 GCT AAT GGA AAC GAC ACT AGT GAT GAC AGT AAT GCT TTA CAA AGA GCA     426
96 Ala Asn Gly Asn Asp Thr Ser Asp Asp Ser Asn Ala Leu Gln Arg Ala
97             60                  65                  70
99 ATT AAT GCT ATT AGT AGA AAA CCG AAT GGG GGC ACT TTA CTA ATA CCG     474
100 Ile Asn Ala Ile Ser Arg Lys Pro Asn Gly Gly Thr Leu Leu Ile Pro
101         75                  80                  85
103 AAT GGA ACT TAC CAT TTC CTC GGC ATA CAG ATG AAG TCG AAC GTA CAC     522
104 Asn Gly Thr Tyr His Phe Leu Gly Ile Gln Met Lys Ser Asn Val His
105         90                  95                  100
107 ATC CGT GTT GAG AGT GAC GTG ATA ATC AAG CCA ACG TGG AAT GGG GAT     570
108 Ile Arg Val Glu Ser Asp Val Ile Ile Lys Pro Thr Trp Asn Gly Asp
109 105                 110                 115                 120
111 GGC AAA AAC CAC CGA CTA TTT GAA GTT GGC GTA AAC AAT ATT GTA AGA     618
112 Gly Lys Asn His Arg Leu Phe Glu Val Gly Val Asn Asn Ile Val Arg
113                 125                 130                 135
115 AAC TTC AGC TTT CAA GGG TTA GGA AAC GGT TTT TTG GTG GAT TTT AAA     666
116 Asn Phe Ser Phe Gln Gly Leu Gly Asn Gly Phe Leu Val Asp Phe Lys
117             140                 145                 150
119 GAT TCT CGC GAC AAA AAC TTA GCT GTT TTT AAG TTA GGC GAT GTT AGA     714
120 Asp Ser Arg Asp Lys Asn Leu Ala Val Phe Lys Leu Gly Asp Val Arg
121         155                 160                 165
123 AAT TAC AAA ATT TCC AAT TTT ACC ATT GAT GAT AAT AAA ACG ATA TTT     762
124 Asn Tyr Lys Ile Ser Asn Phe Thr Ile Asp Asp Asn Lys Thr Ile Phe
125     170                 175                 180
127 GCC TCA ATT TTA GTG GAC GTA ACA GAA CGT AAT GGG CGG TTA CAT TGG     810
128 Ala Ser Ile Leu Val Asp Val Thr Glu Arg Asn Gly Arg Leu His Trp
129 185                 190                 195                 200
131 TCG CGT AAT GGA ATT ATC GAA AGA ATA AAA CAA AAT AAC GCT TTG TTC     858
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132 Ser Arg Asn Gly Ile Ile Glu Arg Ile Lys Gln Asn Asn Ala Leu Phe
133              205              210              215
135 GGC TAC GGC CTT ATT CAA ACC TAT GGC GCA GAT AAT ATT TTG TTT AGG      906
136 Gly Tyr Gly Leu Ile Gln Thr Tyr Gly Ala Asp Asn Ile Leu Phe Arg
137              220              225              230
139 AAC CTC CAT TCG GAA GGC GGA ATT GCG TTA CGG ATG GAA ACT GAC AAC      954
140 Asn Leu His Ser Glu Gly Gly Ile Ala Leu Arg Met Glu Thr Asp Asn
141          235              240              245
143 TTA CTT ATG AAA AAT TAT AAG CAA GGC GGA ATA AGA AAC ATC TTT GCT     1002
144 Leu Leu Met Lys Asn Tyr Lys Gln Gly Gly Ile Arg Asn Ile Phe Ala
145      250              255              260
147 GAT AAT ATC AGA TGT AGC AAA GGA CTT GCG GCG GTC ATG TTT GGC CCA     1050
148 Asp Asn Ile Arg Cys Ser Lys Gly Leu Ala Ala Val Met Phe Gly Pro
149 265              270              275              280
151 CAT TTT ATG AAG AAT GGA GAT GTG CAA GTG ACC AAT GTC AGC TCA GTT     1098
152 His Phe Met Lys Asn Gly Asp Val Gln Val Thr Asn Val Ser Ser Val
153              285              290              295
155 AGT TGC GGT TCG GCT GTA CGA AGT GAT AGT GGA TTT GTC GAA CTC TTT     1146
156 Ser Cys Gly Ser Ala Val Arg Ser Asp Ser Gly Phe Val Glu Leu Phe
157              300              305              310
159 AGC CCG ACA GAC GAA GTA CAT ACG CGT CAA AGT TGG AAA CAA GCC GTT     1194
160 Ser Pro Thr Asp Glu Val His Thr Arg Gln Ser Trp Lys Gln Ala Val
161          315              320              325
163 GAA AGT AAA TTG GGC CGA GGG TGT GCG CAA ACC CCT TAT GCT AGA GGT     1242
164 Glu Ser Lys Leu Gly Arg Gly Cys Ala Gln Thr Pro Tyr Ala Arg Gly
165      330              335              340
168 AAT GGT GGT ACA CGG TGG GCG GCT CGC GTA ACA CAA AAA GAC GCG TGT     1290
169 Asn Gly Gly Thr Arg Trp Ala Ala Arg Val Thr Gln Lys Asp Ala Cys
170 345              350              355              360
172 TTA GAT AAA GCA AAA CTG GAA TAT GGA ATA GAG CCT GGT TCA TTT GGC     1338
173 Leu Asp Lys Ala Lys Leu Glu Tyr Gly Ile Glu Pro Gly Ser Phe Gly
174              365              370              375
176 ACG GTT AAA GTC TTT GAT GTT ACA GCG CGT TTT GGT TAT AAC GCA GAT     1386
177 Thr Val Lys Val Phe Asp Val Thr Ala Arg Phe Gly Tyr Asn Ala Asp
178              380              385              390
180 CTT AAA CAG GAC CAG CTA GAC TAC TTT TCT ACA TCC AAC CCT ATG TGC     1434
181 Leu Lys Gln Asp Gln Leu Asp Tyr Phe Ser Thr Ser Asn Pro Met Cys
182          395              400              405
184 AAG CGT GTA TGC CTT CCT ACA AAA GAA CAA TGG AGT AAG CAA GGC CAA     1482
185 Lys Arg Val Cys Leu Pro Thr Lys Glu Gln Trp Ser Lys Gln Gly Gln
186      410              415              420
188 ATT TAC ATT GGT CCG TCA TTA GCT GCA GTA ATT GAT ACC ACA CCT GAA     1530
189 Ile Tyr Ile Gly Pro Ser Leu Ala Ala Val Ile Asp Thr Thr Pro Glu
190 425              430              435              440
192 ACT TCA AAA TAC GAT TAT GAT GTG AAA ACT TTT AAC GTC AAA AGA ATA     1578
193 Thr Ser Lys Tyr Asp Tyr Asp Val Lys Thr Phe Asn Val Lys Arg Ile
194              445              450              455
196 AAT TTT CCT GTA AAT TCA CAC AAG ACT ATC GAC ACG AAT ACT GAA AGT     1626
197 Asn Phe Pro Val Asn Ser His Lys Thr Ile Asp Thr Asn Thr Glu Ser
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198              460              465              470
200 AGC CGT GTC TGC AAT TAT TAC GGT ATG TCC GAA TGC TCC AGC AGT CGA     1674
201 Ser Arg Val Cys Asn Tyr Tyr Gly Met Ser Glu Cys Ser Ser Ser Arg
202          475              480              485
204 TGG GAG CGA TAGATTAAGC CGCTATATTC ATTTACTAGG TAAAACTTCA             1723
205 Trp Glu Arg
206      490
208 AGCCGCATTC GAAGAACTAT CGAACGCGGC TTTTTTGTTA AGAGCGCCTA TGACTCAGTA   1783
209 TATTTTGTAT AAATATAATT TTACATCTTG TTAAAGTAAA CATCATATGT TTATATAGGT   1843
210 GCAATCTAAT TTGTTAATAT AGTGTTGGAG ATAGGT ATG AAA GGT GTT TCT ACG     1897
211                                    Met Lys Gly Val Ser Thr
212                                                      495
215 AAA AAT GCT CTT TTA TTT GCA GGC TTT TCG TTA AGT CTA GTT GCA CAG     1945
216 Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala Gln
217          500              505              510
219 TCA GTT AGT GCA CAA GAA GCA AAA CAG CCT GAA AAA GAA GAA AAA GAT     1993
220 Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys Asp
221      515              520              525
223 GTT GAG GTG ATT TTG GTA TCG GCA CAA AAG CGT GAG CAA GCG CTT AAA     2041
224 Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu Lys
225 530              535              540              545
227 GAA GTG CCT GTA TCA ATT GAA GTT ATT CAA GGC GAC CTT CTA GA         2085
228 Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu
229              550              555
232 (2) INFORMATION FOR SEQ ID NO: 2:
234      (i) SEQUENCE CHARACTERISTICS:
235          (A) LENGTH: 559 amino acids
236          (B) TYPE: amino acid
237          (D) TOPOLOGY: linear
239      (ii) MOLECULE TYPE: protein
241      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
243 Met Arg Leu Tyr Phe Arg Lys Leu Trp Leu Thr Asn Leu Phe Leu Gly
244   1               5              10              15
245 Gly Ala Leu Ala Ser Ser Ala Ala Ile Gly Ala Val Ser Pro Lys Thr
246              20              25              30
247 Tyr Lys Asp Ala Asp Phe Tyr Val Ala Pro Thr Gln Gln Asp Val Asn
248          35              40              45
249 Tyr Asp Leu Val Asp Asp Phe Gly Ala Asn Gly Asn Asp Thr Ser Asp
250      50              55              60
251 Asp Ser Asn Ala Leu Gln Arg Ala Ile Asn Ala Ile Ser Arg Lys Pro
252 65              70              75              80
253 Asn Gly Gly Thr Leu Leu Ile Pro Asn Gly Thr Tyr His Phe Leu Gly
254              85              90              95
255 Ile Gln Met Lys Ser Asn Val His Ile Arg Val Glu Ser Asp Val Ile
256          100             105             110
257 Ile Lys Pro Thr Trp Asn Gly Asp Gly Lys Asn His Arg Leu Phe Glu
258          115             120             125
259 Val Gly Val Asn Asn Ile Val Arg Asn Phe Ser Phe Gln Gly Leu Gly
260          130             135             140
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263 Asn Gly Phe Leu Val Asp Phe Lys Asp Ser Arg Asp Lys Asn Leu Ala
264 145             150             155         160
265 Val Phe Lys Leu Gly Asp Val Arg Asn Tyr Lys Ile Ser Asn Phe Thr
266             165             170             175
267 Ile Asp Asp Asn Lys Thr Ile Phe Ala Ser Ile Leu Val Asp Val Thr
268             180             185             190
269 Glu Arg Asn Gly Arg Leu His Trp Ser Arg Asn Gly Ile Ile Glu Arg
270         195             200             205
271 Ile Lys Gln Asn Asn Ala Leu Phe Gly Tyr Gly Leu Ile Gln Thr Tyr
272     210             215             220
273 Gly Ala Asp Asn Ile Leu Phe Arg Asn Leu His Ser Glu Gly Gly Ile
274 225             230             235             240
275 Ala Leu Arg Met Glu Thr Asp Asn Leu Leu Met Lys Asn Tyr Lys Gln
276             245             250             255
277 Gly Gly Ile Arg Asn Ile Phe Ala Asp Asn Ile Arg Cys Ser Lys Gly
278             260             265             270
279 Leu Ala Ala Val Met Phe Gly Pro His Phe Met Lys Asn Gly Asp Val
280         275             280             285
281 Gln Val Thr Asn Val Ser Ser Val Ser Cys Gly Ser Ala Val Arg Ser
282     290             295             300
283 Asp Ser Gly Phe Val Glu Leu Phe Ser Pro Thr Asp Glu Val His Thr
284 305             310             315             320
285 Arg Gln Ser Trp Lys Gln Ala Val Glu Ser Lys Leu Gly Arg Gly Cys
286             325             330             335
287 Ala Gln Thr Pro Tyr Ala Arg Gly Asn Gly Gly Thr Arg Trp Ala Ala
288             340             345             350
289 Arg Val Thr Gln Lys Asp Ala Cys Leu Asp Lys Ala Lys Leu Glu Tyr
290         355             360             365
291 Gly Ile Glu Pro Gly Ser Phe Gly Thr Val Lys Val Phe Asp Val Thr
292     370             375             380
293 Ala Arg Phe Gly Tyr Asn Ala Asp Leu Lys Gln Asp Gln Leu Asp Tyr
294 385             390             395             400
295 Phe Ser Thr Ser Asn Pro Met Cys Lys Arg Val Cys Leu Pro Thr Lys
296             405             410             415
297 Glu Gln Trp Ser Lys Gln Gly Gln Ile Tyr Ile Gly Pro Ser Leu Ala
298             420             425             430
299 Ala Val Ile Asp Thr Thr Pro Glu Thr Ser Lys Tyr Asp Tyr Asp Val
300         435             440             445
301 Lys Thr Phe Asn Val Lys Arg Ile Asn Phe Pro Val Asn Ser His Lys
302     450             455             460
303 Thr Ile Asp Thr Asn Thr Glu Ser Ser Arg Val Cys Asn Tyr Tyr Gly
304 465             470             475             480
305 Met Ser Glu Cys Ser Ser Ser Arg Trp Glu Arg Met Lys Gly Val Ser
306             485             490             495
307 Thr Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala
308             500             505             510
310 Gln Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys
311             515             520             525
312 Asp Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/988,201**

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TIME: 19:00:25

Input Set : **N:\Crf3\RULE60\09988201.raw**
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L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]